

GenCore version 5.1.4\_p5\_4578  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 20, 2003, 06:52:11 ; Search time 1 Seconds  
(without alignments)  
0.436 Million cell updates/sec

**-22-3**

Title: us-09-854-280-3

Perfect score: 1073

Sequence: 1 MTLPLGLFLTLWLHTCLAH.....FHTEFIHPVVGCTCVLPKSV 197

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1 seqs, 1107 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=soft -Q=us-09-854-280-3 -DB=us-09-480-297a-22  
-SUFFIX=pt0 -OUT=align\_3\_22 -MINMATCH=0.1 -LOOPCL=0 -LOPEXT=0 -UNITS=bits  
-START=1 -END=1 -MATRIX=BIOSUM62 -TRANS=human40.cdi -LIST=1 -DOCALIGN=200  
-THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=1 -MODE=LOCAL -OUTFMT=pt0  
-NORM=ext -HEAPSIZE=500 -MINLEN=2000000000 -NCP0=6 -NO\_XLPXY  
-NEG\_SCORES=0 -LONGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : us-09-480-297a-22:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1073	100.0	1107	1	us-09-480-297a-22

#### ALIGNMENTS

RESULT 1  
us-09-480-297a-22

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
0	1073.00	100.00%	100.00%	100.00%	1	1107	197	0	0	0	0

us-09-854-280-3 (1-197) x us-09-480-297a-22 (1-1107)

Qy	1	MetThrLeuLeuProGlyLeuLeuPheLeuThrTrpLeuHisThrCysLeuAlaHisHis	20
Db	115	ATGACGCTCTCCCGGCTCTCTGTTCTGACCTGGCTGCACACATGCTGGCCGCCCAT	174

Qy	21	AspProSerLeuArgGlyHisProHisSerHisGlyThrProHisCysTyrSerAlaGlu	40
Db	175	GACCCCTCCCTCAGGGGACCCACACAGTCCAGTACCCACACTGCTACTCGGCTAG	234
Qy	41	GluLeuProLeuGlyGlnAlaProProHisLeuLeuAlaArgGlyAlaLysTrpGlyGln	60
Db	235	GAACCTGCCCTCGGCGAGGCCCCACACCTGCTGGCTCGAGTGCCCAAGTGGGGCAG	294
Qy	61	AlaLeuProValAlaLeuValSerSerLeuGluAlaAlaSerHisArgGlyArgHisGlu	80
Db	295	GCTTGGCTGTAGCCCTGGTGTCCAGCTGGAGGACCAAGCCACAGGGGGAGCCACGAG	354
Qy	81	ArgProSerAlaThrThrGlnCysProValLeuArgProGluGluValLeuGluAlaAsp	100
Db	355	AGGCCCTCAGCTACGCCAGTCCCGGTGCTGGCGCGGAGGAGGTGTTGGAGGCAGAC	414
Qy	101	ThrHisGlnArgSerIleSerProTrpArgTyrArgValAspThrAspGluAspArgTyr	120
Db	415	ACCCACGACGCTCCATCTCACCTGAGATACCGTGTGGACACGGATGAGGACCGCTAT	474
Qy	121	ProGlnLysLeuAlaPheAlaGluCysLeuCysArgGlyCysIleAspAlaArgThrGly	140
Db	475	CCACAGAGCTGGCTTCCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGACGGGC	534
Qy	141	ArgGluThrAlaAlaLeuAsnSerValArgLeuLeuGlnSerLeuValLeuArgArg	160
Db	535	CGCGAGACAGCTGGCTCACTCCGCGGCTGCTCCAGAGCCCTGCTGGTGTGGCGGC	594
Qy	161	ArgProCysSerArgAspGlySerGlyLeuProThrProGlyAlaPheAlaPheHisThr	180
Db	595	CGGCCCTGCTCCCGACGGCTCGGGGCTCCCCACACCTGGGGGCTTTGCTTCCACACC	654
Qy	181	GluPheIleHisValProValGlyCysThrCysValLeuProArgSerVal	197
Db	655	GAGTTCATCCACGTCGCCGCTCGGCTGCACCTGCGTGTGCCCCCGTTTCAGTG	705

Search completed: May 20, 2003, 06:52:12  
Job time : 1 secs